

1

cgactggagcagcaggacactgacatggactgaaggagtagaaggtttaaaaaaccagtttgagaa ATG TCT AAG TCT GGG CTT CAT CTT  
M S K S G L H L

93  
GTA GCC TAC ATA TTA TTG ATA TTT TTA ATT TCA ACT AAT ATA GCA TCT AAA ATT TCT GGT GTT CCA TTA TGC AAC  
V A Y I L L I F L I S T N I A S K I S G V P L C N

168  
AAA GAT ACT TCA CCA GTA TTT ACA CTT CAA CAT AAT TCT ACT AAT GGT ATT TTA GCT AGA TCT CTT CCA CAA CCA  
K D T S P V F T L Q H N S T N G I L A R S L P Q P

243  
GGA TTA ATT GAT TGT TCA GAA CAT TGT TCC TCT TCG TCA GAT TGT ATT GGC GTT GAA TAT TGG CAG GGA ATT TGT  
G L I D C S E H C S S S S D C I G V E Y W Q G I C

318  
AGA GTT ATT TCT CAA GAT AAA ACT TCT ATT TAT ACA CCA ACA GAT GAA ACT TCA ATA CTT TTA ACA AAA TCA TGT  
R V I S Q D K T S I Y T P T D E T S I L L T K S C

393  
GTT AAA AGT GAT CGT ATA TGT TCA TCA CCA TTC CAT TTT GAT GTT TAT GAA CAA AAA ATA TTA GTT GGA TTT GCT  
V K S D R I C S S P F H F D V Y E Q K I L V G F A

468  
AGA GAA GTT GTA CCA GCT GAG TCT ATT GAA ATT TGT ATG GCT GCT TGT TTG AAT GCT TTT GAT ACA TAT GGT TTT  
R E V V P A E S I E I C M A A C L N A F D T Y G F

543  
GAA TGT GAA TCA GCT ATG TAT TAT CCA GTT GAT AGT GAA TGT ATT CTT AAT ACT GAA GAT AGA CTT GAT CGA CCA  
E C E S A M Y Y P V D S E C I L N T E D R L D R P

618  
GAT CTT TTT GTT GTT GAA AAA GAA GAT GTT GTT TAT TAT CTT GAT TCT AAT TGT GCT GGT TCA CAA TGT TAT GCT  
D L F V V E K E D V V Y Y L D S N C A G S Q C Y A

693  
CCA TAC ATT ACA CAA TAT ATT GCT GTT GAA AAT AAA CAA ATA GAA AAT GAA TTA GAT AGA AAA TTT GAA AAT ATT  
P Y I T Q Y I A V E N K Q I E N E L D R K F E N I

768  
GAT TTC CAA ACA TGT GAA GAA TTA TGT ACT GGT AGA ATT ACT GTT ACA CAA AAT GAT TTT ACT TGT AAA TCA TTT  
D F Q T C E E L C T G R I T V T Q N D F T C K S F

843  
ATG TAT AAT CCT GAA ACA AAA GTT TGT TAT CTT TCT GAT GAA CGT TCA AAG CCT CTT GGA CGG GCT AAA TTA AGT  
M Y N P E T K V C Y L S D E R S K P L G R A K L S

918  
GAT GCT AAT GGA TTT ACT TAT TAT GAA AAA AAA TGT TTT GCA TCT CCA AGA ACA TGC CGT CAA ACA CCA TCA TTT  
D A N G F T Y Y E K K C F A S P R T C R Q T P S F

993  
AAT AGA GTA CCA CAA ATG ATT CTT GTT GGT TTT GCT GCA TTT GTT ATG GAA AAT GTA CCA TCT GTT ACT ATG TGC  
N R V P Q M I L V G F A A F V M E N V P S V T M C

1068  
CTT GAT CAA TGT ACA AAT CCA CCA CCA GAG ACA GGT GAA AAA TTT GTC TGT AAA TCT GTT ATG TAC TAT TAT AAT  
L D Q C T N P P P E T G E K F V C K S V M Y Y Y N

1143  
GAA CAA GAA TGT ATT CTT AAT GCT GAA ACA AGA CAT ACA AAG CCA GAT CTT TTT ATT ACA GAA GGA GAT GAA TTT  
E Q E C I L N A E T R H T K P D L F I T E G D E F

1218  
CTT GTT GAT TAT TTT GAT ATT TCA TGT CAT CTT GAA CCA GAA ACA TGT CCT AAA GGA ACA TAT TTA AAA GGA ATT  
L V D Y F D I S C H L E P E T C P K G T Y L K G I

1293  
AAA TCT ATC AAT TCT GCA CTT CCT GAG GGT GAA GGC TCA CTT CAT GTT ATT GAG TCT GCT GGA AAA TCA TTA GAA  
K S I N S A L P E G E G S L H V I E S A G K S L E

1368  
GAA TGT ATG GAA AAA TGT AAC CAA CTT CAT CCA GAA AAA TGT AGA TCA TTT AAT TTT GAA AAA TCA TCT GGA TTA  
E C M E K C N Q L H P E K C R S F N F E K S S G L

1443  
TGT AAT CTT TTA TAT CTT GAT GGA AAA AAT ACT TTA AAA CCA TTT ATT AAA AAT GGA TTT GAT CTT GTT GAT TTA  
C N L L Y L D G K N T L K P F I K N G F D L V D L

FIGURE 1A

1518  
 CAA TGT TTA TCA ACT AAA AAA GAT TGC TCT ACA AAA AAG AAT GAT ATT AAT TTT GTT AAA TAT CTT TAC TCT CAT  
 Q C L S T K K D C S T K K N D I N F V K Y L Y S H  
 1593  
 TTT GTT AAA TAT CTT TAC TCT CAA CAA CCT GGA ATT CCA ACA AAA ACA GAA AAA GTT ATT GGT ATT TCT AAA TGT  
 F V K Y L Y S Q Q P G I P T K T E K V I G I S K C  
 1668  
 CTT GAT TTA TGT ACT GAT AGT GAA CGT TGT GAA GGA CTT AAT TAT AAT AGA AGA ACT GGA GAA TGT CAA TTA TTT  
 L D L C T D S E R C E G L N Y N R R T G E C Q L F  
 1743  
 GAA ATT ATT GAT GGA CCT TCT AAT CTT AAA AAA TCT GAG CAT ATA GAT TTT TAT CAA AAT CTT TGT TCT ACT AAA  
 E I I D G P S N L K K S E H I D F Y Q N L C S T K  
 1818  
 GAA AAT GAA GCT GGT GTT TCA TCT GCA TTA AAT GTA CCA CAA TCA TCT GTT ATT CCT ATT TCA TCA TCA CAA AAT  
 E N E A G V S S A L N V P Q S S V I P I S S S Q N  
 1893  
 ATT AGT AAA AGT GAT GTT TTT GCC AAA AAA AAT CTT AAT AAA GAT GGT AAT AAT CAA GTA AAC ATT TAT GAA CCA  
 I S K S D V F A K K N L N K D G N N Q V N I Y E P  
 1968  
 GAA AAA AAA TAC CAT CCA AAA GGA TCA AAA AAT GAA ACA TCA TAT GAA ACA GGA ACT GTA AAT AAA TCA AAT GTT  
 E K K Y H P K G S K N E T S Y E T G T V N K S N V  
 2043  
 GAA GAG GTT TCT GAA ACT TTA ACT AAT AGT GGA GTT GAA AGT GGA AGT CTT GAA AAA AAT ATT ATT ACA GCA CCA  
 E E V S E T L T N S G V E S G S L E K N I I T A P  
 2118  
 CCA TCT ATA CCA AAA ATT CCT GAA GGT CCA CTA CCA GTG CCA ATT TTA ATT CCA GCT GAT CAA GTA CAA ACT ATT  
 P S I P K I P E G P L P V P I L I P A D Q V Q T I  
 2193  
 TGT GAT TAT GAA GGT ATT AAA GTA CAA ATT AAA TCA CCA CAA TCA TTT ACT GGT GTT ATC TTT GTT AAA AAT CAC  
 C D Y E G I K V Q I K S P Q S F T G V I F V K N H  
 2268  
 TAT GAA ACA TGT CGT GTT GAA GTT TCC AAC TCT GAT GCA GCT ACT CTT GAG CTT GGT CTT CCA GCT TCA TTT GGA  
 Y E T C R V E V S N S D A A T L E L G L P A S F G  
 2343  
 ATG AAA CCA GTT ACA CTG TCT GCT ACA TCT TCA GAT TCT ACC TCT TCA CAG AAT ATT ACT TCT AAT AGT GGA CAT  
 M K P V T L S A T S S D S T S S Q N I T S N S G H  
 2418  
 AAA GTT GTT GGA AGA GCA CGC CGT GAT ACA CAA GAA AAA TCT TGT GGT CTT ACA GAA ATT GAA AAT GGA AAA TAT  
 K V V G R A R R D T Q E K S C G L T E I E N G K Y  
 2493  
 AAA AGT ACT GTT GTT ATA CAA ACA AAT AAC CTT GGA ATT CCT GGA CTT GTA ACA TCA ACA GAT CAA ATT TAT GAA  
 K S T V V I Q T N N L G I P G L V T S T D Q I Y E  
 2568  
 ATT GGT TGT GAT TAT AGT AGT ATG TTA GGA GGA AAA ATT ACT ACA GCA GCT AAT ATG ACT GTA AAT GGA CCA ACA  
 I G C D Y S S M L G G K I T T A A N M T V N G P T  
 2643  
 CCA ACT GAT ATT AAA CCT AGA GGT AAA ATT GAA CTT GGA AAT CCT GTT CTT ATG CAA ATG AAT GCT GGT ACA GGT  
 P T D I K P R G K I E L G N P V L M Q M N A G T G  
 2718  
 GAT CAT CAG CCA ATT TTA CAA GCT AAA CTT GGA GAT ATT CTT GAA TTA AGA TGG GAA ATT ATG GCT ATG GAT GAA  
 D H Q P I L Q A K L G D I L E L R W E I M A M D E  
 2793  
 GAA CTT GAT TTC TTT GTT AAA GAT TGT CAT GCA GAA CCT GGT ACT GGT GCT GGA GGA GAT GAA AAA CTT CAG CTT  
 E L D F F V K D C H A E P G T G A G G D E K L Q L  
 2868  
 ATT GAA GGT GGA TGC CCA ACA CCA GCT GTT GCT CAA AAA CTT ATT CCA CAA CCA ATA AAA TTA CAA TCA TCA GCT  
 I E G G C P T P A V A Q K L I P Q P I K L Q S S A  
 2943  
 GTC AAA ATT GCC CAT CTT CAA GCT TTC CGT TTT GAT TCA TCC TCT TCA GTT AGA ATA ACA TGT AAT ATT GAA ATT  
 V K I A H L Q A F R F D S S S S V R I T C N I E I  
 3018  
 TGT AAG GGA GAT TGT AAA CCA GCA ACA TGT GAT ATG CAC GGA GAA TCA AAA CAA TCA TGG GGA AGA AAA AAG AGA  
 C K G D C K P A T C D M H G E S K Q S W G R K K R  
 3093  
 CAT ATT GAA GAT GAT ACA ATT ACA GAA TTT GAG ACA AAT CGT TAT AAA GTT CCA AGA TTT TCA CAA GCA ACA ACA  
 H I E D D T I T E F E T N R Y K V P R F S Q A T T

FIGURE 1B

Applicant(s): Michele Coutu Hresko et al.

## NEMATODE PAN AND ZP RECEPTOR-LIKE SEQUENCES

3168

TCT CTT TTA ATT CTT GAT CCA CTT CAA AAT AAC ATT GAA CCA GCA TCA TTA ATG TCA AAA GTA TCA TCT CTT GAT  
S L L I L D P L Q N N I E P A S L M S K V S S L D

3243

TTG TTA GCT GAA GAT CCT GCA AAA ACA TTA CTT AAG ATT AAA GAG ACT GCA CAT TTG AAT GGA AAT CTT TGT ATG  
L L A E D P A K T L L K I K E T A H L N G N L C M

3318

GGA AAA ATT ACA CTT TTC TCA GTA TTT GGT GTT CTT CTT TCA TTA ATT GTT GTT CAA GCA ATT GTC GTA ACA AAT  
G K I T L F S V F G V L L S L I V V Q A I V V T N

3393

TAT ATT TTT AAA AGA GTT ATG TCA AGC AGA AAG ATT ACC AAT TAAactttaataattaacaataattataaatatgcctttatgt  
Y I F K R V M S S R K I T N

3479

tctcaaaacgagtataatcctttttttggttattaatttttagtatcaaaatatatataccgatggcatttacaataataataaatacaactgaagaaag

3579

ctataatatgaaaccgtgccagaaacttattcaaagtttttaattctctctctctctcttttctaatttcctttcaaaacattccattttttttttgttt

3679

ttatttaatacaaaaataataattaatagtaatttatgatatatcattaatatttttataatatttttttg

FIGURE 1C

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1
ggcacgagaa  ATG AAC TGG CTA TCT ATA GCT TCA ATT TGT ACA TTC TTA ATT ATA CCA ATA TCT GCT GTC TTT GAA
      M   N   W   L   S   I   A   S   I   C   T   F   L   I   I   P   I   S   A   V   F   E

77
TGT TCA GGA TCA GAA ACT ACA GCA TTT ATT AGA ATA TCC AGA GCA CGC CTT GAT GGG ACA CCA GTA GTT ATT TCT
C   S   G   S   E   T   T   A   F   I   R   I   S   R   A   R   L   D   G   T   P   V   V   I   S

152
ACA GCA GGA CAT GAC TTG ACT TGT GCA CAA TAT TGT AGA AAT AAT ATT GAA CCA ACA ACT GGT GCT CAA CGT GTC
T   A   G   H   D   L   T   C   A   Q   Y   C   R   N   N   I   E   P   T   T   G   A   Q   R   V

227
TGT GCA TCA TTT AAT TTT GAT GGT CGT GAA ACA TGC TAC TTT TTT GAT GAT GCT GCC TCA CCT GCT GGG ACT GGG
C   A   S   F   N   F   D   G   R   E   T   C   Y   F   F   D   D   A   A   S   P   A   G   T   G

302
GAG TTG AAT GAA GCA CCA TCA GCT AAT AAT TTT TAT TAT GAA AAA GTT TGC CTT CCA GCT ATC TCT GCT CAT GAA
E   L   N   E   A   P   S   A   N   N   F   Y   Y   E   K   V   C   L   P   A   I   S   A   H   E

377
GCA TGT ACT TAT AGA TCA TTT TCA TTT GAA AGA ACT AGA AAT ACT CAA TTA GAA GGT TTT GTT AAA AAA TCA CTA
A   C   T   Y   R   S   F   S   F   E   R   T   R   N   T   Q   L   E   G   F   V   K   K   S   L

452
CAA GTT ACA TCA CGT GAA GAA TGC CTT TCT ACA TGT TTA AAA GAA AGT GAA TTT GTA TGT AGA TCA GTT AAC TAT
Q   V   T   S   R   E   E   C   L   S   T   C   L   K   E   S   E   F   V   C   R   S   V   N   Y

527
AAT TAT GAA AAC TTT ATG TGT GAA CTT TCA ACA GAA AGA TCG CGT TCT AAA CCA CAA AAT ATG AGA ATG TCA GCA
N   Y   E   N   F   M   C   E   L   S   T   E   R   S   R   S   K   P   Q   N   M   R   M   S   A

602
GCT CCA GTT GAT TAT TAT GAT AAT AAT TGT TTA AAT AGA CAA AAT AGA TGT GGT GAA TCT GGT GGA AAT TTG ATT
A   P   V   D   Y   Y   D   N   N   C   L   N   R   Q   N   R   C   G   E   S   G   G   N   L   I

677
TTT ATT AAA ACA ACA CAA TTT GAA ATT CAT TAT TAT GAT CAT ACT CAA TCA ATG GAA GCA CAA GAA TCA TTC TGT
F   I   K   T   T   Q   F   E   I   H   Y   Y   D   H   T   Q   S   M   E   A   Q   E   S   F   C

752
TTA CAA AAA TGT TTA GAT TCA TTA AAC ACC TTC TGT AGA TCT GTT GAA TAT TCT CCA TCT GAA AAA AAT TGT ATT
L   Q   K   C   L   D   S   L   N   T   F   C   R   S   V   E   Y   S   P   S   E   K   N   C   I

827
GTT TCT GAT GAA GAT ACA TAT TCA AGA GCT GAT CAA CAA GGT GAA GTT AAT AAT AAA GAT TAT TAT GAA CCT GTT
V   S   D   E   D   T   Y   S   R   A   D   Q   Q   G   E   V   N   N   K   D   Y   Y   E   P   V

902
TGT GTT GCT GCT GAT CTT AGT TCA TCT ACA TGT CGT CAA CAA GCT GCT TTT GAA AGA TTT ATT GGT TCT GCT ATT
C   V   A   A   D   L   S   S   S   T   C   R   Q   Q   A   A   F   E   R   F   I   G   S   A   I

977
GAA GGT ACC CCA GTT GCT ACA GCA CAA CAA GTA ACC ATT TCT GAT TGT ATT TCA CTT TGT TTC CAA AAT TTG AAT
E   G   T   P   V   A   T   A   Q   Q   V   T   I   S   D   C   I   S   L   C   F   Q   N   L   N

1052
TGT AAA TCA ATT AAT TAT GAT CGT ACA CAA TCT ACA TGT TAT ATT TAT GCT GTT GGA AGA CAA GAA TCT AAT GTT
C   K   S   I   N   Y   D   R   T   Q   S   T   C   Y   I   Y   A   V   G   R   Q   E   S   N   V

1127
AAA AAT GAT GCA AGT TTC GAT TAT TAT GAA TTT ACA ATT ATT GAT AAT GGA TGC CCA AGA TAT CCT GCT CTT GTA
K   N   D   A   S   F   D   Y   Y   E   F   T   I   I   D   N   G   C   P   R   Y   P   A   L   V

1202
GGG CCA GTT TTA CAA GAT TTC GAC AAA AAT CGT CTT AAA TCT GAA ATG AAA GCA TTC CGT TTA GAT GGA TCA TAT
G   P   V   L   Q   D   F   D   K   N   R   L   K   S   E   M   K   A   F   R   L   D   G   S   Y

1277
GAT ATT CAA ATT GAA TGT TCT GTT ATG TTT TGT GCT GGT CCA ATG GGT TGT CCA CCA TCT AAT TGC CTT GAT TCA
D   I   Q   I   E   C   S   V   M   F   C   A   G   P   M   G   C   P   P   S   N   C   L   D   S

1352
GGA ACA AAT GAA TTA TTT GCT TCA CAT GGA AGA AAG AAA AGA AGT ATT GTT GAT TTC AAA AAT ACA ACA ACA TCT
G   T   N   E   L   F   A   S   H   G   R   K   K   R   S   I   V   D   F   K   N   T   T   T   S

1427
GCA GAA ACA TTA TCT GCT ATA ATT AGA GTA CTT GCT GCT GGA GAA GAA GAA TTA GAA GTT GAA GAA TTT TAT AGA
A   E   T   L   S   A   I   I   R   V   L   A   A   G   E   E   E   L   E   V   E   E   F   Y   R

1502
AAT GAT ACT AAT TTT AAA TAT GAT TCT GAA GAA AAT ATC TCA GCT CAT AAC TTA TAC TGT ATG TCT GAA ATG TGG
N   D   T   N   F   K   Y   D   S   E   E   N   I   S   A   H   N   L   Y   C   M   S   E   M   W

```

FIGURE 2A

1577

TTT GTA TCA GGA ATT GTT TCA ATG GCT ATG ATC TGT CTT CTT CTT TCT GTT CTT ATA GTT ATG TGG GGC TGT CAT  
F V S G I V S M A M I C L L L S V L I V M W G C H

1652

TCA TTA AAT CAA TCT TCA AAA TTA CCA ATG TGAaggaagatctttcaacaaaaaaaaacgattaatttttaatatttctttaatatatac  
S L N Q S S K L P M

1742

attccataatcagtatataactataataattgcaacataataattttattgtagaagtctgtttataaaatcaaatcacaaatttttcttttacagtactgt  
1842

gcacaacaacaagaaattccaatctcttcctatatattttgatgtcgtacacacgtttataaaaaacaaattcttttggttttaacagttttcagttttaca  
1942

tttatataat

FIGURE 2B

Applicant(s): Michele Coutu Hresko et al.

## NEMATODE PAN AND ZP RECEPTOR-LIKE SEQUENCES

1  
 gcgtcgatagtcgattttttaagggtttaattacccaagcttaaggaatatttgaagcttatttttaagaaaaataaattaaataagagattagcaca

101  
 acaacaacagaaatttttcttgaattttacaacaaaataattttttcttaattaaattccttttaattatccacaacttct ATG GTT ACA AAA ATC  
 M V T K I

196  
 CCA ACT TTT CCC CTC CTT TTT ATT TTC CCA TTT TTA TTT ACA TTT TTA ACG ACA AAA TGT CAG GCT TAT TCT ATA  
 P T F P L L F I F P F L F T F L T T K C Q A Y S I

271  
 CCA TTA ATA TCA GAA TGT AAT TCG GAA GAA GCC CCA GTT TTT CTT TTG CAA CGG AAT GTT TCT TCT ATC GCC GGA  
 P L I S E C N S E E A P V F L L Q R N V S S I A G

346  
 ACT GAG CCT TTA AGA ACT GTT CCT GTT ACA GGG GGA TTT TTG GAA TGT GCG GAA CTT TGT TCA GCA GCA AAT AAT  
 T E P L R T V P V T G G F L E C A E L C S A A N N

421  
 TGT GTT GCT GTT AAA TTT TCT ATT GAA AAA CAA TGC CAA TTG TTG GGG AAA ACA ACT ATG ACA GCA ACA ACT TTA  
 C V A V K F S I E K Q C Q L L G K T T M T A T T L

496  
 TCT TTA CAA GAC ATT AAT TTG ACA CTA GCT AGA TTA GCT ACT AAA AGT TGT GTT AAG AGC AAA AAA ATC TGT TCT  
 S L Q D I N L T L A R L A T K S C V K S K K I C S

571  
 TCC CCC TTC CAT TTT GAT GTT CAC GAA CAA AAA ATA CTT GTT GGT TTT GCT AGA GAA GTT GTA TCA GCA GAA TCT  
 S P F H F D V H E Q K I L V G F A R E V V S A E S

646  
 ATA CAT CAA TGT TTA ACT GCT TGT TTA GAT GCT GTT GAT ACT TTT GGC TTT GAA TGC GAG TCA GTA ATG TAT TAT  
 I H Q C L T A C L D A V D T F G F E C E S V M Y Y

721  
 CCA TTG GAT GCC GAA TGT ATT TTA AAT ACA GAA GAC AGA CTT GAC CGT CCA GAT TTG TTT GTT GAT GAG AAG GAA  
 P L D A E C I L N T E D R L D R P D L F V D E K E

796  
 GAT ACT GTT GTT TAT TTG GAT AAT AAT TGT GCT GGA TCC CAA TGT CAT GCC CCT TAT GTA ACC CAA TAT GTA GCT  
 D T V V Y L D N N C A G S Q C H A P Y V T Q Y V A

871  
 GTT GAA GGA AAA CAA TTA GCT GAG GAA TTG GAT CAT AAT TTT GAG GGA ATG GAG TTG ACA GAA TGT GAA CAG CTT  
 V E G K Q L A E E L D H N F E G M E L T E C E Q L

946  
 TGT AAT CAA AGA TTG AGT GTT TCT GCA AAT GAC TTT AAT TGC AAA GCA TTT ATG TAC AAT AAC CAA ACA AGA TCT  
 C N Q R L S V S A N D F N C K A F M Y N N Q T R S

1021  
 TGT ATT CTT TCT GAT GAA CGT TCA AGA CCT TTG GGT AGA GCT AAT TTG ACA GAT GCT AAA GGA TGG ACT TAT CAC  
 C I L S D E R S R P L G R A N L T D A K G W T Y H

1096  
 GAG AAA AAA TGT TTT GCC TCC CCA CGT ACA TGC CGA AAT GTT CCT TCT TTT ACC CGC GTC CCT CAA ATG TTA TTA  
 E K K C F A S P R T C R N V P S F T R V P Q M L L

1171  
 GTT GGA TTT GCC TCT TTT GTA ATG GAA AAT GTC CCT TCA GTA ACT ATG TGT TTG GAT CAA TGT ACA AAT CCT CCC  
 V G F A S F V M E N V P S V T M C L D Q C T N P P

1246  
 CCA GAA ACT GGA CAA AGT TTT GTT TGT AAA TCT GTC ATG TAT TAT TAT AAT GAG CAA GAA TGT ATT TTA AAT GCT  
 P E T G Q S F V C K S V M Y Y Y N E Q E C I L N A

1321  
 GAA TCA CGT CAT TCC AAG CCA GAT TTA TTT ATT CCC GAA GAA GAC GAT TTT GTT GTA GAT TAT TTT GAT ATA AAT  
 E S R H S K P D L F I P E E D D F V V D Y F D I N

1396  
 TGC CGT CTA GAA CAA GAA CAA TGT ATC GAT GGA AGA ACG CCC CAA TTA GTT AGA ACA ATT AAT TCT GCA CTT CCA  
 C R L E Q E Q C I D G R T P Q L V R T I N S A L P

1471  
 GAA GGG GAG GGG TCT ATA CAT GTT TTG GAA ACA ATT AAG GGA GGA GTT CAG CAA TGT GCT AAA AAA TGT TCT GAA  
 E G E G S I H V L E T I K G G V Q Q C A K K C S E

1546

FIGURE 3A

CGC GCC CCA GAC AAA TGT CGC TCT TTC AAT TTT GAT AAA CAA GCT GGT AAT TGT AAT TTA CTT TAT TTG GAT GGA  
 R A P D K C R S F N F D K Q A G N C N L L Y L D G  
 1621  
 CAA GGG TCT TTA CGA CCA GAG CAA AAG ACA CAA TTC GAT TTA TAC GAT GTT CAT TGT TTG AGT GGA ACA TCT CAA  
 Q G S L R P E Q K T Q F D L Y D V H C L S G T S Q  
 1696  
 CTT TTA GGA GAA AAT TCT AAA CAT TCT CCC TCT GCT TGT GTT GAC CCA GAA GGG GCT ATT TTT AGT CGT TTC CTC  
 L L G E N S K H S P S A C V D P E G A I F S R F L  
 1771  
 TAC ACT CGT TGG GTA GCA AAT TCT CCC AAT CGT GAA ATT TCA AGT TTA CCA CTT TCC AAA TGT TTA AAT CTT TGT  
 Y T R W V A N S P N R E I S S L P L S K C L N L C  
 1846  
 TCG GTT GGA GGA GAA CAA TGT GAG GGT GTT AAT TAC AAT CGC CGA AAT GGT TCT TGT CAA TTA TTT ACT TCC CTT  
 S V G G E Q C E G V N Y N R R N G S C Q L F T S L  
 1921  
 CTA TTA AAC TCT TCT CCA AAT TCT CAA CAA GAC AAA GAC GAA CAT GTT GAT TTT TAC AGA AAT ATT TGT AGA GTT  
 L L N S S P N S Q Q D K D E H V D F Y R N I C R V  
 1996  
 AAG GAA TCG AAA AGT GAT AGT GGG GCT GCT AAT GTA CCC AAA ACA CAA CAA GCA ACG GCT GCA CCT CCC CCT TCT  
 K E S K S D S G A A N V P K T Q Q A T A A P P P S  
 2071  
 GTT CAA TTA ACT ACT AAA CCT CCA CAA ATT CGT GAT TTA AAC AAC AAC AAT AAA ACA ACA CAC AAA GAA CCA AAT  
 V Q L T T K P P Q I R D L N N N N K T T H K E P N  
 2146  
 ATT AAA CTT CCA CCA CAA TCA GCA AAA CCT ATA AAT GGA AAA ACT GGA AAG GAA CAA CTT CCT GTA GGG TCA AAA  
 I K L P P Q S A K P I N G K T G K E Q L P V G S K  
 2221  
 TCT TTT GGG GTT ACT AAT ACG CGT GAT GAT GGG GAG AAT TCA ATA ACT GGA ACT GCT CCT CCT CCT GTA GAT GGC  
 S F G V T N T R D D G E N S I T G T A P P P V D G  
 2296  
 AAA TTA ATT ATT AAA CCT TCA CCA CAA GTT TCT ATT CCC TCC CCT GTA CTT ATT CCG GCA CAA GAA GTA CAT ACT  
 K L I I K P S P Q V S I P S P V L I P A Q E V H T  
 2371  
 ATT TGT AAT TAT GAA GGA ATT AGT GTT CAA ATT AAA CAT TCT TCT CCA TTC TCT GGC GTT GTT TTT GTT CGA AAT  
 I C N Y E G I S V Q I K H S S P F S G V V F V R N  
 2446  
 AAA TAT GAT ACT TGC CGT GTG AAG TTG AAG GAA AGG ACA GCG TTG TTT TGG TTT TGG GGC TTC CAG CAA ATT TTG  
 K Y D T C R V K L K E R T A L F W F W G F Q Q I L  
 2521  
 GAA ATG AAG CCA ATT GCT TTA ATT AAT TCA CAA AAA CAT GGA AAA GGG AAT AAA ACA CAC GGA GAT ACT TTA CTT  
 E M K P I A L I N S Q K H G K G N K T H G D T L L  
 2596  
 TCT ATT GAA GGT TCC AAA AAA CAA ATT GAA GGG GGT TCT TCA ACT GAA GAT ATT CAA TTA ATA AAT TCT CAA AAA  
 S I E G S K K Q I E G G S S T E D I Q L I N S Q K  
 2671  
 GAC CTT AAA CGT TCA AGA AGA CAA TTA CAA AGA GAT TGT GGA TTA CAA GAT ATG GAC AAT GGA ACT TAC AAA ACT  
 D L K R S R R Q L Q R D C G L Q D M D N G T Y K T  
 2746  
 GTT ATT GTT GTC CAA ACA AAT AAT TTG GGA ATT CCG GGA CTT GTT ACT TCT ATG GAC CAA CTT TAT GAG ATT TCC  
 V I V V Q T N N L G I P G L V T S M D Q L Y E I S  
 2821  
 TGT AAC TAT TCA AGT ATG TTG GGA GGC AAA GTC CAA ACA GCA GCT GCA TTA CGT GTT CAC GGT CCC CAA CCT TCA  
 C N Y S S M L G G K V Q T A A A L R V H G P Q P S  
 2896  
 CTA ATC CAG CCT CGC GGC AAA ATA GAA TTG GGA AAT CCT GTT TTG ATG CAA ATG GGG CCT GTA CGT AGT GAA AGG  
 L I Q P R G K I E L G N P V L M Q M G P V R S E R  
 2971  
 CAA AGT GGG GAA GGG CCT TTA ATT CAA GCT AAA TTG GGG GAT ATT CTT GAA TTA AAA TGG GAA ATT ATG GCA ATG  
 Q S G E G P L I Q A K L G D I L E L K W E I M A M  
 3046  
 GAT GAA GAA TTG GAC TTT TTA GTT CGT GAT TGT TTT GCA GAG CCG GGA ACT TCT GGA AAT CAA GGG GAA AGA CTT  
 D E E L D F L V R D C F A E P G T S G N Q G E R L

FIGURE 3B

Applicant(s): Michele Coutu Hresko et al.

## NEMATODE PAN AND ZP RECEPTOR-LIKE SEQUENCES

3121  
CCT TTA ATT GAG AAT GGT TGT CCA ACA CCA GCA GTA GCA CAA AAA TTA ATT CCA AAT CCA ATA AAA GCA ATT AAT  
P L I E N G C P T P A V A Q K L I P N P I K A I N  
3196  
TCT GCA GTT AAA TTA ACT TAT TTA CAA GCA TTC AGA TTT GAC AGT TCT CCA GCT ATT AGA ATA ACT TGT CAT TTA  
S A V K L T Y L Q A F R F D S S P A I R I T C H L  
3271  
GAA TTA TGT AAA GAA AAT TGT AAA TCG GTT AAT TGT AAA TTT AAT GAT GGA ATT AAA GAA TCG TGG GGC AGA AAA  
E L C K E N C K S V N C K F N D G I K E S W G R K  
3346  
CGC CGT TTT GCT ATT GAC AAT AAC ATT AAT AGG AAA AAT GAA GTT AAA GAA TTC GAA ACT CGC CGT TTT GTC GTT  
R R F A I D N N I N R K N E V K E F E T R R F V V  
3421  
CCC CGT TTT GCC CAA GCA ACA ACT TCT TTA GTT ATT GTA GAC CCT TTA CAA CAA CAA AAT TCT GTT ATA AAA ACA  
P R F A Q A T T S L V I V D P L Q Q Q N S V I K T  
3496  
GAA CAA CAA CAA CAA CCA TTT ATT TCA CAT TCC TCA ATA TCT AAA CAA ATA TTT GAA AAT AAT AAA AAA GAA AAT  
E Q Q Q Q P F I S H S S I S K Q I F E N N K K E N  
3571  
AAT AAA AAT ATA ACA AAA ACA GCT AAA AAA TCC TCT TCT CTT TTT GAA GCT TTT ACT GAG GCT GCT GGT GGA AGG  
N K N I T K T A K K S S S L F E A F T E A A G G R  
3646  
AAA ATT AAT TTA GAA TTA ACA ACA ACA AAT TCA GAA CAA CAA CAA CTT TGT TTA CAT AAA TGG ACA CTT GGG GGT  
K I N L E L T T T N S E Q Q Q L C L H K W T L G G  
3721  
GTT TTT GGA ACT CTT TTA ACA TTA ATT GTT GTT CAA AGC GGG GTT GCT GCT AAA CAT TTA ATT AAT CGA TTT ATT  
V F G T L L T L I V V Q S G V A A K H L I N R F I  
3796  
GTT GGA AAA AGA ATT TAAaaaaaaaaaaaaaagtactagtcgacgcgtggcc  
V G K R I

FIGURE 3C



1  
GAG CAG AAG ATT TTG GTG GGT TTC GCG CGG GAG GTG GTC TCC GCC GAC TCA GTC CAC CGC TGT CTG  
E Q K I L V G F A R E V V S A D S V H R C L  
67  
TCC GCT TGT CTG AAT GCG TTC GAT ACG TTC GGC TTC GAA TGC GAG TCG GTC ATG TAT TAC CCT GTG GAC GCG GAA  
S A C L N A F D T F G F E C E S V M Y Y P V D A E  
142  
TGC ATT TTG AAC ACG GAG GAC CGA TTG GAT CGG CCT GAC CTT TTC GTG GAC GAG CAC GAG GAC ACG GTC ATC TAC  
C I L N T E D R L D R P D L F V D E H E D T V I Y  
217  
TTG GAC AAC AAT TGC GCC GGA TGT GAG TGC CAT TGG CAT TTT GAC AAT TTC AAA ACA AGC GGC ATT TTG AAC GAC  
L D N N C A G C E C H W H F D N F K T S G I L N D  
292  
CAA CAA TTC GCA ATT GCA GCA CAA TGT TAC GCA CCG TAC GTA ACG CAA TAC GTG GCG GTG GAA GGA CGC CAA TTG  
Q Q F A I A A Q C Y A P Y V T Q Y V A V E G R Q L  
367  
TCG GAC GAA TTG GAC CAC AGT TTT GAA GGG TTG GAG CTG AGC GAA TGT GAA GAG TTG TGC ACG CAA CGG TTA AGT  
S D E L D H S F E G L E L S E C E E L C T Q R L S  
442  
GTT ACG GCA AAC GAC TTC AAC TGC AAA TCG TTC ATG TAC AGT AAC TTG ACG CGC AGT TGC GTT TTG TCG GAC GAA  
V T A N D F N C K S F M Y S N L T R S C V L S D E  
517  
CGC TCG CGC CCT TTG GGC CGT GCC AAT TTG GCC GAA GTG CCG GGA TGG ACT TAT TTC GAG AGC CGC GGC GTT CCG  
R S R P L G R A N L A E V P G W T Y F E S R G V P  
592  
TCG TTT ACG CGA GTG CCG CAA ATG CTT TTG GTG GGC TTT GCC TCT TTT GTG ATG GAA AAT GTG CCG TCA GTG ACA  
S F T R V P Q M L L V G F A S F V M E N V P S V T  
667  
ATG TGT TTG GAC CAA TGC ACA AGC CCT CCT CCT GAG ACG GGA CAA AAC TTT GTG TGT AAA TCG GTG ATG TAC TAC  
M C L D Q C T S P P P E T G Q N F V C K S V M Y Y  
742  
TAC AAC GAG CA  
Y N E

FIGURE 4

1  
cgactggagcagcaggacactgacatggactgaaggagtagaaaatttctgttgttcatttcttatcagactgtcccattcatcatcgtagaccactacca  
101  
gtattacttcaggacagtaatattcggttaaatttcggtgctcaatcggtaggaccgctttaat ATG CAT CTT TCC AAC CAT GCC TCA  
M H L S N H A S  
190  
TCA CTT CTG CAT TAC TAT TCA CAT CTC ATC ATA ATT GCA TAC TTT TCT GTA TTT GCT TCA ATC GAA ATA CAA GAA  
S L L H Y Y S H L I I I A Y F S V F A S I E I Q E  
265  
ATT CCA TCA TAT CCA GCA TGT AGC AAT GGC GAA TCA CCT GTC TTT TTA CTC CAA CAC AAT GCT ACA GCA GGT AAT  
I P S Y P A C S N G E S P V F L L Q H N A T A G N  
340  
GTT CTG AAG CGA GCT TCA ACT TCA CAT CTG GTC GAC TGC ACT GAC CTT TGT TCA GCT AAC GAT GAA TGT TTG GCG  
V L K R A S T S H L V D C T D L C S A N D E C L A  
415  
ATA ACC TAT GAA GAT AAA GAA TGC AAA ATG TTG TCA AGC ATT GGA GAA TCG ACA GGA CAT TTA AAT GAT TAT GTA  
I T Y E D K E C K M L S S I G E S T G H L N D Y V  
490  
TTG CTG AGT AAA AAT TGT GCT AAA AGT GCG CGG ATC TGC TCA TCG CCA TTT CAA TTC GAT GTA CAC AGA CAA AAA  
L L S K N C A K S A R I C S S P F Q F D V H R Q K  
565  
ATT TTG GTT GGG TTT GCT CGC GAG GTT GTG TCA GCT GAT TCA TTA TCG TTA TGT CTA TCA GCT TGC TTG AAT GCA  
I L V G F A R E V V S A D S L S L C L S A C L N A  
640  
TTT GAT TCT TTC GGT TTT GAA TGT GAG TCG GTA ATG TAC TAT CCA GTT GAT TCA GAA TGC ATC CTA AAC ACC GAA  
F D S F G F E C E S V M Y Y P V D S E C I L N T E  
715  
GAT CGT CTG GAT CGA CCT GAC TTG TTT GGG GAT GAA TTA GAT GAT AAC GTC ATT TAT TTG GAT AAC AAC TGT GCT  
D R L D R P D L F G D E L D D N V I Y L D N N C A  
790  
GGA TCA CAG TGT TAT GCT CCA TAC ATA ACA CAA TAC ATT GCC GTC GCA AAT CGT CAG CTA GCT AAC GAG TTG GAC  
G S Q C Y A P Y I T Q Y I A V A N R Q L A N E L D  
865  
AGA CAA CTG ATC GCT GAT CGT GAA TCA TGC GAG TCG TTA TGT ACT CAG CGA CTG TCT ACA ACG ACA AAC GAT TTC  
R Q L I A D R E S C E S L C T Q R L S T T T N D F  
940  
AAC TGT AAA TCA TTT ATG CAT AAT CCG GAA ACT AAC GTT TGC ATA CTT TCT GAT GAA CGT TCT AAA CCA CTT GGT  
N C K S F M H N P E T N V C I L S D E R S K P L G  
1015  
CGA GGC AAT CTA GTG AAA GCT GAC GGT TTC ACA TAT TAT GAG AAG AAA TGT TTT GCA TCA CCA CGA ACA TGT CGC  
R G N L V K A D G F T Y Y E K K C F A S P R T C R  
1090  
AAT GTA CCG TCG TTT GAG CGC ATA CCT CAG ATG ATA CTT GTT GGT TTT GCT GCA TTT GTT ATG GAA AAT GTA CCT  
N V P S F E R I P Q M I L V G F A A F V M E N V P  
1165  
TCA GTA ACG ATG TGC CTC GAT CAG TGC ACA AAT CCT CCA CCG GAA ACT GGA GAA AAT TTC GAA TGC AAA TCT GTG  
S V T M C L D Q C T N P P P E T G E N F E C K S V  
1240  
ATG TAT TAT TAT AAC GAA CAG GAA TGT ATT TTA AAC GCT GAA ACA CGA GAA AAT AAA TCG GAA TTG TTT ATA CCG  
M Y Y Y N E Q E C I L N A E T R E N K S E L F I P  
1315  
GAG GGA GAA GAA TTC CAA GTC GAT TAT TTT GAT ATC ACT TGT CAT CTG CGC CCT GAA ACA TGT CCA AAT GGC ACA  
E G E E F Q V D Y F D I T C H L R P E T C P N G T  
1390  
ACA TTA CAT ACT GTA CGT ACG GTT AAT GCA GCA CTC CCT GAA GGC GAA GGA TCG ATC CAT ATT TTG CAG TCA GCC  
T L H T V R T V N A A L P E G E G S I H I L Q S A  
1465  
GGG AAT TCG GTT GCT GAT TGC ATG ACA AAA TGT TAC GAG ATG GCT CCC GAG AAA TGT CGC GCA TTC AAT TTT GAT  
G N S V A D C M T K C Y E M A P E K C R A F N F D

FIGURE 5A

1540  
AAG CAG ACA TCT GAC TGT GAC CTG CTG TAC GTT GAT GGG AAG ACA ACC TTA CGA CCA GCA GTC CAC TCG GGC ATT  
K Q T S D C D L L Y V D G K T T L R P A V H S G I

1615  
GAT CTC TAC GAC CTT CAT TGC CTA GAG CAG ACA AAA GTT TGC GCT CAG AAA AAC AAC GTA ACA CGA TTT TCG AGA  
D L Y D L H C L E Q T K V C A Q K N N V T R F S R

1690  
TAT TTG TAC AGT ATA TAT GAT GCA GTG CCA TCG CAA TTC TAC GAA GCA ACT GCC CTC ACA AAT TGT CTT AAT CTT  
Y L Y S I Y D A V P S Q F Y E A T A L T N C L N L

1765  
TGC GCA TAT ACC GAG CGT TGC GAA GGT GTA AAT TAC AAC AGA AGG AAT GGT CGT TGT GAA TTA TTT GAT AAG GTC  
C A Y T E R C E G V N Y N R R N G R C E L F D K V

1840  
GAA GGA AAT GGA AAG CCA AGT GAT TTC ACG GAT TTT TAC AAA AAT CTT TGT CTG GTG GAA GAA GTA GAA TCA GAA  
E G N G K P S D F T D F Y K N L C L V E E V E S E

1915  
TAT AGC GCC GCA GCT AAT GTT CCC AAA CAT CTC CTT CCG AAT GTT TCA CAT TCT GCA GTT ACT CAG AAA CAA GAA  
Y S A A A N V P K H L L P N V S H S A V T Q K Q E

1990  
GCT AAA TTA CAC ATT ATC TCA GCA AAA ACA AAG CCT TTC CTA CGC GAA CAG GAA GCA CAG CGA CGA GCT CCA GAA  
A K L H I I S A K T K P F L R E Q E A Q R R A P E

2065  
ACA ATA ACA GCG AAG TCG TCT TCA GCT TCC GGA AAA GTA AGT GGT GAA GCA GGA TCA TCA ACT ACA TTC AGC ATT  
T I T A K S S S A S G K V S G E A G S S T T F S I

2140  
TCT TCA TCC GGA AGG CTT CCA GGG CCA GTA GTC CAA ATT GCT CCA AAT GCA GTG CAA ACA GTT TGC AAT TAT GAA  
S S S G R L P G P V V Q I A P N A V Q T V C N Y E

2215  
GGC ATC AAA GTG CAG ATG GAG AAC CCC AAA GCC TTT TCG GGA GTG ATA TTT GTT AAA AAT AGG TAT GAA ACC TGT  
G I K V Q M E N P K A F S G V I F V K N R Y E T C

2290  
CGA GTA GAG GTT ACG GAT AGT GAA AGT GCA CCA CTA GTA ATT GGT TTA CCA CCG AAT TTT GGT TCA AAA ATG GTA  
R V E V T D S E S A P L V I G L P P N F G S K M V

2365  
GCT GAT GAA AAG GTT GCC GCA AGC GAA GCA AAT ATT CAA CCA GAA ATA TCC GGA GGC GAC AAA CTG GAT AAA CCC  
A D E K V A A S E A N I Q P E I S G G D K L D K P

2440  
GCT GAT GAA CTG CGC ATA AGA CGA CAA GCT TTA GAG CTA CAC AGA GAT TGC GGA ATC CAG GAT ATG AAC AAT GGT  
A D E L R I R R Q A L E L H R D C G I Q D M N N G

2515  
ACT TAT AAA TCA ACG GTG GTT GTA CAA ACA AAT AAC TTG GGT ATA CCT GGA CTG GTA ACT TCC ATG GAT CAG ATT  
T Y K S T V V V Q T N N L G I P G L V T S M D Q I

2590  
TTT GAA GTG AGC TGT GAT TAT AGT TCA ATG CTT GGT GGA AAA GTT ACT GCT GGT GCC AAT CTC ACA ATT GAT GGT  
F E V S C D Y S S M L G G K V T A G A N L T I D G

2665  
CCC GAA GCA TCT CTT ATT CAA CCC CGA GGA AAA ATC GAA CTT GGT AAC CCG GTG CTT ATG CAG ATG TTG AGT GGA  
P E A S L I Q P R G K I E L G N P V L M Q M L S G

2740  
CAA GGA GAA CCT GTC CTA CAA GCA AAA CTA GGT GAC ATT CTG CAG CTA CGA TGG GAA ATC ATG GCG ATG  
Q G E P V L Q A K L G D I L Q L R W E I M A M

FIGURE 5B

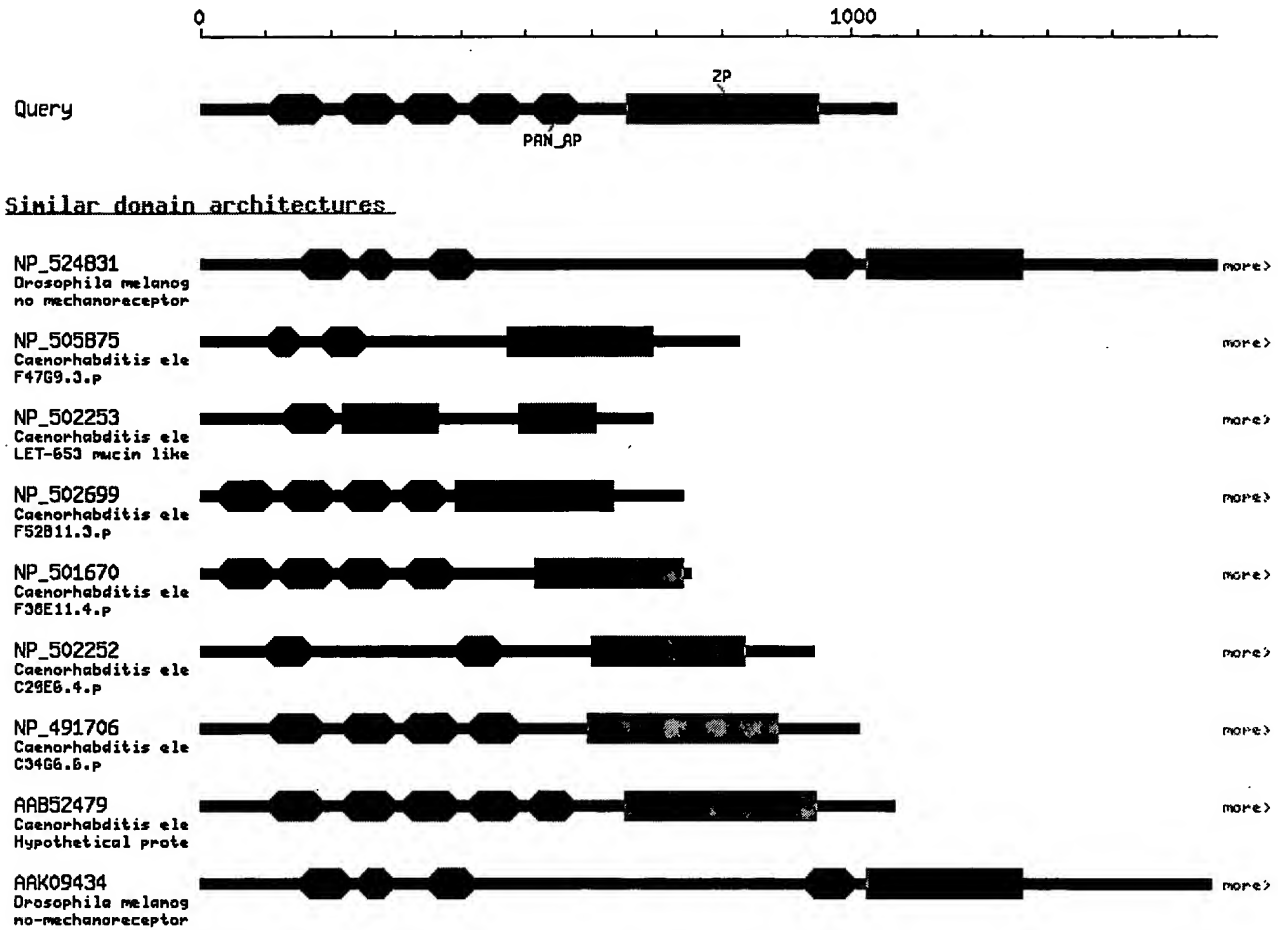


FIGURE 6

SEQ ID No 10	MYTRIPTFELLVIFPFLFTLTKCA	---YSIPLISECNSSEAPVFLIQNVSSTAGTEPLRTVPVTGGLECBELCSAANNCAVAFPSIEKQCQLLQKTTMTATTLBQDINHLARLAKSCVKS	126
SEQ ID No 11	-----	-----	-----
SEQ ID No 16	-----MKVFAVLAALVAVSGLA	-----DTLPSVTLCPPEPTQTFIYVLOEN-----TTVG-ARIRTIPTSE-LAECSDHCSASLDCQGVFK-DGSCAVFBAOSE-----KATAGS-----QLLTKTCVKS	101
SEQ ID No 17	-----MKVFAVLAALVAVSGLA	-----DTLPSVTLCPPEPTQTFIYVLOEN-----TTVG-ARIRTIPTSE-LAECSDHCSASLDCQGVFK-DGSCAVFBAOSE-----KATAGS-----QLLTKTCVKS	101
SEQ ID No 45	-----MKVFAVLAALVAVSGLA	-----DTLPSVTLCPPEPTQTFIYVLOEN-----STVG-ARIRTIPTSE-LAECSDHCSASLDCQGVFK-DGSCAVFBAOSE-----KATAGS-----QLLTKTCVKS	101
SEQ ID No 3	-----MSKSGSLVAYILLIFLSTNIA	-----SKISGVPLCKNDSTSPVFLLOEN-----STVG-ILARSLEPQG-LIDCSHCSASSDCIGVETM-QGICRVIISQKDTGITPTDRTS-----ILLTKTCVKS	112
SEQ ID No 12	MELSNHASSLEYSLLIAYFVSVAEISIQEISYPACSNHGSFVFLLOEN	-----ATAGNVLEK-----ASTSHLVCTDLCSANDCLATYSE-DKECKMLSSIGES-----TGLHNDY-----VLLSKNCAKSA	118
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130		
SEQ ID No 10	KICSSPFHVDHREKQILVGFARFVVSADSVHRCISACLNADFTTGFCECSVMYTPVDAECILNTEDELRDPLFVDEKEDTVYLDNNCAG	-----SQCHAFYITQYVAVE	232
SEQ ID No 11	-----EQKILVGFARFVVSADSVHRCISACLNADFTTGFCECSVMYTPVDAECILNTEDELRDPLFVDEKEDTVYLDNNCAG	-----SQCHAFYITQYVAVE	118
SEQ ID No 16	RVCSPPFDLFSQKILVGFARFVVAANIQICMAACLNADFTTGFCECSAMFTYVDQECILNTEDELRDPLFVDEKEDTVYLDNNCAGFPFLVFN	-----YNYQKTTFSKSCQYFFIITQYIAVE	224
SEQ ID No 17	RVCSPPFDLFSQKILVGFARFVVAANIQICMAACLNADFTTGFCECSAMFTYVDQECILNTEDELRDPLFVDEKEDTVYLDNNCAGFPFLVFN	-----YNYQKTTFSKSCQYFFIITQYIAVE	224
SEQ ID No 45	RVCSPPFDLFSQKILVGFARFVVAANIQICMAACLNADFTTGFCECSAMFTYVDQECILNTEDELRDPLFVDEKEDTVYLDNNCAGFPFLVFN	-----YNYQKTTFSKSCQYFFIITQYIAVE	224
SEQ ID No 3	RICSSPFHVDHREKQILVGFARFVVSADSVHRCISACLNADFTTGFCECSAMFTYVDQECILNTEDELRDPLFVDEKEDTVYLDNNCAG	-----SQCHAFYITQYIAVE	218
SEQ ID No 12	RICSSPFHVDHREKQILVGFARFVVSADSVHRCISACLNADFTTGFCECSAMFTYVDQECILNTEDELRDPLFVDEKEDTVYLDNNCAG	-----SQCHAFYITQYIAVE	218
ruler	.....140.....150.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260		
SEQ ID No 10	GKQLAEHLNDFRQMLTECRQLCNQLSVSANDFNCAKAFMYNNQTRSCILSDERSRPLGRANLDAKGMTTHKKCFASPTCRNVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	-----SRGVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	362
SEQ ID No 11	GRQLSELDHSEFGLSECEBLCTQRLSVTANDFNCKSFMYNNKTRTCILADERSKPLGRADLAEVPMQWTF	-----SRGVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	239
SEQ ID No 16	GKQLNELDR-IINVDLSCQALCTQRLSISNDFNCKSFMYNNKTRTCILADERSKPLGRADLAEVPMQWTF	-----SRGVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	353
SEQ ID No 17	GKQLNELDR-IINVDLSCQALCTQRLSISNDFNCKSFMYNNKTRTCILADERSKPLGRADLAEVPMQWTF	-----SRGVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	353
SEQ ID No 45	GKQLNELDR-IINVDLSCQALCTQRLSISNDFNCKSFMYNNKTRTCILADERSKPLGRADLAEVPMQWTF	-----SRGVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	353
SEQ ID No 3	NKQENELDRKFENIDFQCEBLCTQRLSISNDFNCKSFMYNNKTRTCILADERSKPLGRADLAEVPMQWTF	-----SRGVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	348
SEQ ID No 12	NKQENELDR-IINVDLSCQALCTQRLSISNDFNCKSFMYNNKTRTCILADERSKPLGRADLAEVPMQWTF	-----SRGVPSFTTRVPMQLLVGFASFVMEVSVTMCCLDQCTNPPPTQGSF	353
ruler	.....270.....280.....290.....300.....310.....320.....330.....340.....350.....360.....370.....380.....390		
SEQ ID No 10	VCKSVMYTNEQECILNASTREKSLFIPRGEFVVDYFDINCRLEQEQCIDGRTPOLVRTINSALPREGESIHVLET-IGGVQVQCAKCKSERAPDKCRSFNFDKQAGNCNLLYLDGQGSLEPQKTQ	-----AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	491
SEQ ID No 11	VCKSVMYTNEQECILNASTREKSLFIPRGEFVVDYFDINCRLEQEQCIDGRTPOLVRTINSALPREGESIHVLET-IGGVQVQCAKCKSERAPDKCRSFNFDKQAGNCNLLYLDGQGSLEPQKTQ	-----AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	250
SEQ ID No 16	VCKSVMYTNEQECILNASTREKSLFIPRGEFVVDYFDINCRLEQEQCIDGRTPOLVRTINSALPREGESIHVLET-IGGVQVQCAKCKSERAPDKCRSFNFDKQAGNCNLLYLDGQGSLEPQKTQ	-----AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	483
SEQ ID No 17	VCKSVMYTNEQECILNASTREKSLFIPRGEFVVDYFDINCRLEQEQCIDGRTPOLVRTINSALPREGESIHVLET-IGGVQVQCAKCKSERAPDKCRSFNFDKQAGNCNLLYLDGQGSLEPQKTQ	-----AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	483
SEQ ID No 45	VCKSVMYTNEQECILNASTREKSLFIPRGEFVVDYFDINCRLEQEQCIDGRTPOLVRTINSALPREGESIHVLET-IGGVQVQCAKCKSERAPDKCRSFNFDKQAGNCNLLYLDGQGSLEPQKTQ	-----AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	483
SEQ ID No 3	VCKSVMYTNEQECILNASTREKSLFIPRGEFVVDYFDINCRLEQEQCIDGRTPOLVRTINSALPREGESIHVLET-IGGVQVQCAKCKSERAPDKCRSFNFDKQAGNCNLLYLDGQGSLEPQKTQ	-----AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	477
SEQ ID No 12	VCKSVMYTNEQECILNASTREKSLFIPRGEFVVDYFDINCRLEQEQCIDGRTPOLVRTINSALPREGESIHVLET-IGGVQVQCAKCKSERAPDKCRSFNFDKQAGNCNLLYLDGQGSLEPQKTQ	-----AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	482
ruler	.....400.....410.....420.....430.....440.....450.....460.....470.....480.....490.....500.....510.....520		
SEQ ID No 10	FDLYDVHCLSG---TSQQLGENSKHSPS---ACVDPGAIFSRFLYTRVWAMSPNRIBSLPLSKCNLNCVSGGQECGVNYYNRNRSQCLFTSLNNSPNSQDQDEHVPFYANICRVKRSKS-DSGA	-----RHTDFYKNCVTKRIDTGASAA	614
SEQ ID No 11	-----	-----	250
SEQ ID No 16	VDLYDLHCLIA---VENDCSANIDD---ALFSRYLHTK---QRGIPAKYVYVLSNLSCLFVC-AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	-----RHTDFYKNCVTKRIDTGASAA	588
SEQ ID No 17	VDLYDLHCLIA---VENDCSANIDD---ALFSRYLHTK---QRGIPAKYVYVLSNLSCLFVC-AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	-----RHTDFYKNCVTKRIDTGASAA	592
SEQ ID No 45	VDLYDLHCLIA---VENDCSANIDD---ALFSRYLHTK---QRGIPAKYVYVLSNLSCLFVC-AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	-----RHTDFYKNCVTKRIDTGASAA	591
SEQ ID No 3	VDLYDLHCLIA---VENDCSANIDD---ALFSRYLHTK---QRGIPAKYVYVLSNLSCLFVC-AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	-----RHTDFYKNCVTKRIDTGASAA	592
SEQ ID No 12	VDLYDLHCLIA---VENDCSANIDD---ALFSRYLHTK---QRGIPAKYVYVLSNLSCLFVC-AGNPTCAGANNRRLDCTFLDAIDDDAHIN-----RHTDFYKNCVTKRIDTGASAA	-----RHTDFYKNCVTKRIDTGASAA	587
ruler	.....530.....540.....550.....560.....570.....580.....590.....600.....610.....620.....630.....640.....650		
SEQ ID No 10	ANVPKTOQAT---AAPPSPVQLTKK---PPQIRDLNN---NNKTTHEKPNIKLPPQ---SAKPIKNGTKQKGLPVGSKSPGVNTRDDG	-----NTE-HRRAPES	691
SEQ ID No 11	ANVPKTOQAT---AAPPSPVQLTKK---PPQIRDLNN---NNKTTHEKPNIKLPPQ---SAKPIKNGTKQKGLPVGSKSPGVNTRDDG	-----NTE-HRRAPES	250
SEQ ID No 16	ANVPKTOQAT---AAPPSPVQLTKK---PPQIRDLNN---NNKTTHEKPNIKLPPQ---SAKPIKNGTKQKGLPVGSKSPGVNTRDDG	-----NTE-HRRAPES	634
SEQ ID No 17	ANVPKTOQAT---AAPPSPVQLTKK---PPQIRDLNN---NNKTTHEKPNIKLPPQ---SAKPIKNGTKQKGLPVGSKSPGVNTRDDG	-----NTE-HRRAPES	638
SEQ ID No 45	ANVPKTOQAT---AAPPSPVQLTKK---PPQIRDLNN---NNKTTHEKPNIKLPPQ---SAKPIKNGTKQKGLPVGSKSPGVNTRDDG	-----NTE-HRRAPES	637
SEQ ID No 3	LNVPQSSVIP---SSSQNLSKS---DVPAKKNLNDG---NQVNYIEPEKKYHPK---GSK-NETSETGTGTVKNSNVEVSTLTG-	-----GSK-NETSETGTGTVKNSNVEVSTLTG-	667
SEQ ID No 12	ANVPKTOQAT---AAPPSPVQLTKK---PPQIRDLNN---NNKTTHEKPNIKLPPQ---SAKPIKNGTKQKGLPVGSKSPGVNTRDDG	-----NTE-HRRAPES	651
ruler	.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750.....760.....770.....780		
SEQ ID No 10	ENSGTGTAPFP---VDGKLLIKSPQVSPISPLVPAQGVETICNYEGISVQIKHSSPFSGVVFNKTYDTCRVKLEKERTALFPMWPGQQLIEKPIALINSQKHG	-----PVEVKARATQTCNYESGIVQVNNNGEPFSGVIFVKNHFTDCRVVANSNAATLVGLQKDFGMRIBLNDINDNE	794
SEQ ID No 11	-----	-----	250
SEQ ID No 16	-----	-----	715
SEQ ID No 17	-----	-----	719
SEQ ID No 45	-----	-----	718
SEQ ID No 3	SGVBSGLSKN---ITTPATBIPKIPGFLPVLPIDPADQVQTCNYESGIVQVNNNGEPFSGVIFVKNHFTDCRVVANSNAATLVGLQKDFGMRIBLNDINDNE	-----PVEVKARATQTCNYESGIVQVNNNGEPFSGVIFVKNHFTDCRVVANSNAATLVGLQKDFGMRIBLNDINDNE	771
SEQ ID No 12	-----	-----	742
ruler	.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900.....910		
SEQ ID No 10	KGKNTHG---DTLLSIEGSKKIQEGSSST-EDIQILNSQKDLKRSRRQLQ-RDCGLQMDMNGYTKTVVQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	-----STPLKDEISEFPQKROAAEFPRDCGLVLLNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	918
SEQ ID No 11	-----	-----	250
SEQ ID No 16	TKGKK---TKGKE---STPLKDEISEFPQKROAAEFPRDCGLVLLNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	-----STPLKDEISEFPQKROAAEFPRDCGLVLLNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	823
SEQ ID No 17	TKGKK---TKGKE---STPLKDEISEFPQKROAAEFPRDCGLVLLNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	-----STPLKDEISEFPQKROAAEFPRDCGLVLLNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	827
SEQ ID No 45	TKGKK---TKGKE---STPLKDEISEFPQKROAAEFPRDCGLVLLNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	-----STPLKDEISEFPQKROAAEFPRDCGLVLLNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	826
SEQ ID No 3	TSQN---TS-NSGHELVGARRDTQKSCGLTIEHNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	-----TS-NSGHELVGARRDTQKSCGLTIEHNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	827
SEQ ID No 12	ANIQP---RISGG---DKLDKPADELIRIRQAELH-RDCGQMDMNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	-----RISGG---DKLDKPADELIRIRQAELH-RDCGQMDMNGYTKSTVVIQTNHIGPLVTSMDQLYBISCNYSMLGGQVQTAALREHVGPPQLIOPRKGIELGNP	850
ruler	.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040		
SEQ ID No 10	VLMQMPVRSERQSGEGLIQAQGLDILELRWEINAMDELDFFVKNCHAEFPGVAGGKAGAGKRLIDGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	-----AGGDEKLLQIEGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	1045
SEQ ID No 11	-----	-----	250
SEQ ID No 16	VLMQGLN---GDQTEQPLVQAQGLDILELRWEINAMDELDFFVKNCHAEFPGVAGGKAGAGKRLIDGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	-----AGGDEKLLQIEGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	949
SEQ ID No 17	VLMQGLN---GDQTEQPLVQAQGLDILELRWEINAMDELDFFVKNCHAEFPGVAGGKAGAGKRLIDGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	-----AGGDEKLLQIEGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	953
SEQ ID No 45	VLMQGLN---GDQTEQPLVQAQGLDILELRWEINAMDELDFFVKNCHAEFPGVAGGKAGAGKRLIDGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	-----AGGDEKLLQIEGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	952
SEQ ID No 3	VLMQGLN---GDQTEQPLVQAQGLDILELRWEINAMDELDFFVKNCHAEFPGVAGGKAGAGKRLIDGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	-----AGGDEKLLQIEGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	996
SEQ ID No 12	VLMQGLN---GDQTEQPLVQAQGLDILELRWEINAMDELDFFVKNCHAEFPGVAGGKAGAGKRLIDGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	-----AGGDEKLLQIEGGCPTPAVAQKLIPGAIKISAVKTTMQAFRFDSSASIKVTCFVEICKGDCBPVECALT	881
ruler	.....1050.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170		
SEQ ID No 10	DGICKSWGKRFPADNNINNRKNEVKEFETRRFVPRFAQATTSLVIVDPLQQQNSVIKTEQQQQPFISSHSISKQIPENKKNKNNKNTAKKSSSLFRAFTAAAGGRKINLELITTSNQQLCLHK	-----ITSEFETNRYLIPRSHATTSTIVIDPLQQVNEPV-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	1175
SEQ ID No 11	-----	-----	250
SEQ ID No 16	GGVKSFGKRRKRVSNH---ITSEFETNRYLIPRSHATTSTIVIDPLQQVNEPV-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	1030
SEQ ID No 17	GGVKSFGKRRKRVSNH---ITSEFETNRYLIPRSHATTSTIVIDPLQQVNEPV-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	1034
SEQ ID No 45	GGVKSFGKRRKRVSNH---ITSEFETNRYLIPRSHATTSTIVIDPLQQVNEPV-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	1033
SEQ ID No 3	GESQSWGKRKHIEDDT---ITSEFETNRYLIPRSHATTSTIVIDPLQQVNEPV-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	-----AMSRATLIDLREH-AHRVQMIEH-----GSLCLNS	1085
SEQ ID No 12	-----	-----	881
ruler	.....1180.....1190.....1200.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300		
SEQ ID No 10	WTLOGVPGTLLTLVIVQSGVAALHNRPIVQKRI---	1210	
SEQ ID No 11	-----	250	
SEQ ID No 16	VTVFAIPGTLAVLLGQTVVIAHYAVRRFSSEKTA---	1065	
SEQ ID No 17	VTVFAIPGTLAVLLGQTVVIAHYAVRRFSSEKTA---	1069	
SEQ ID No 45	VTVFAIPGTLAVLLGQTVVIAHYAVRRFSSEKTA---	1068	
SEQ ID No 3	ITLVSFVGGLSLVIVQAVTVNTYIKRVMSRKITN---	1122	
SEQ ID No 12	-----	881	
ruler	.....1310.....1320.....1330.....		

Figure 7 BEST AVAILABLE COPY

Figure 8